

Outbreak of a new measles B3 variant in the Roma/Sinti population with transmission in the nosocomial setting, Italy, November 2015 to April 2016

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A measles outbreak occurred from November 2015 to April 2016 in two northern Italian regions, affecting the Roma/Sinti ethnic population and nosocomial setting. Overall, 67 cases were reported. Median age of 43 cases in three Roma/Sinti camps was four years, nosocomial cases were mainly adults. The outbreak was caused by a new measles virus B3.1 variant. Immunisation resources and strategies should be directed at groups with gaps in vaccine coverage, e.g. Roma/Sinti and healthcare workers.

Despite a national goal to eliminate measles by 2015, Italy is one of 18 European Region Member States where endemic transmission of measles has not been interrupted [1]. We report here a recent measles outbreak in northern Italy (Figure 1) affecting the Roma/Sinti ethnic population and the nosocomial setting.

Outbreak description

Measles cases were reported to the Italian national integrated measles and rubella surveillance system coordinated by the Istituto Superiore di Sanità in Rome.

Milan clusters (Lombardy region, northern Italy)

The outbreak originated in a nomadic settlement in Milan and then spread to two other settlements in the city. The three settlements house persons of mainly Roma/Sinti ethnic origin but also migrants of various nationalities. A large degree of social interaction occurs between the three camps, as they are inhabited by related family groups.

In total, 43 cases were reported with dates of rash onset from 7 November 2015 to 18 February 2016 (weeks 45/2015 to 7/2016). Figure 2 shows the number of reported measles cases by date of symptom onset. Forty of 43 cases were Roma/Sinti while three were migrants, including one individual from North Africa and two from South Asia. Median age of the 43 cases was four years (range: 5 months–29 years) and 39 were 15 years or younger. Thirty-nine of 43 cases were unvaccinated. Of the four vaccinated cases, three had received post-exposure vaccination in connection with the outbreak.

Twenty-seven cases were laboratory-confirmed and 16 were probable cases [2]. Twelve cases reported complications, including six cases of pneumonia, four cases of diarrhoea and two cases of otitis media. Eighteen cases were admitted to hospital and 14 were seen in the emergency department but not admitted.

Parma and Piacenza clusters (Emilia Romagna region, northern Italy)

The outbreak spread from Lombardy to Emilia Romagna in the cities of Parma (17 cases from 13 January to 13 April) and Piacenza (seven cases from 6 March to 3 April 2016). Here, transmission occurred mainly in the nosocomial setting.

The Parma cluster originated from an unvaccinated adult, employed near a Roma camp in Milan, who was visiting Parma. While there, the patient developed fever in early January 2016 and was hospitalised four days later. Measles was diagnosed after two more

FIGURE 1

Areas involved in a measles outbreak affecting the Roma/Sinti population with transmission in the nosocomial setting, Italy, November 2015–April 2016



days, following rash onset. While hospitalised, the case transmitted the infection to an unvaccinated adult sibling. Two healthcare workers (HCW) in the same hospital and two persons who visited the hospital during the outbreak period also developed measles, although no direct contact with any of the other identified cases was reported. One of the HCW transmitted the infection to another HCW. Other cases related to this cluster included four HCW working in different healthcare settings in the community and six persons with no apparent contact with any of the above cases. All 17 cases were linked virologically. Median age was 37 years (range: 22–49 years). None were vaccinated. One case was complicated by keratoconjunctivitis.

The Piacenza cluster originated from a hospital worker with no direct patient contact, who was hospitalised with high fever over 14 days starting in the first week of March, but in whom a diagnosis of measles was made only retrospectively, after hospital discharge, when four unvaccinated HCW in the same hospital developed measles. Two HCW transmitted the infection to a relative outside the hospital setting. Median age of these seven cases was 40 years (range: 35–68 years). A high rate of complications occurred among cases: three developed pneumonia, two of them with acute respiratory insufficiency, three developed diarrhoea, two keratoconjunctivitis, one pericarditis, one

thrombocytopenia and one Guillain-Barré syndrome. In addition, five of seven cases developed increased liver enzymes. All HCW were admitted to hospital.

Genotyping and phylogenetic analysis

We performed a genetic analysis of measles viruses isolated from 14 of 43 cases from the three Roma camps (respectively, two, 11 and one strain from camps 1, 2 and 3) and 22 of 24 cases from the clusters in Emilia Romagna (respectively, 17 and five cases from the Parma and Piacenza clusters). Phylogenetic analysis based on the available partial nucleoprotein gene sequences showed that all sequences were identical to each other and belonged to genotype B3.1 (Figure 3) [3,4].

BLAST analysis of the World Health Organization's measles nucleotide surveillance (MeaNS) database [5,6] shows that the strain identified represented a new variant of this genotype, first reported in August 2015 (week 32/2015) in Como (Lombardy) and Rimini (Emilia-Romagna), in two cases for whom no epidemiological link was found.

Since August 2015 and up to April 2016, besides the outbreak cases, the new B3 variant has also been identified in other cases with no epidemiological link to the outbreak. In total, it has been identified in 17 non-Roma cases in various cities in Lombardy and four cases in Emilia-Romagna in cities other than Parma and Piacenza (Figure 3).

All sequences are available in the MeaNS database (sequence ID numbers: 86275-86278, 86280-86281, 86283, 86285-86323, 89315-89325) [5,6].

Outside of Italy, identical sequences have been identified in Spain, Germany, and the United Kingdom in August to September 2015 (before the described outbreak, weeks 35–39/2015) and in Romania in January 2016 (week 3/2016).

Control measures

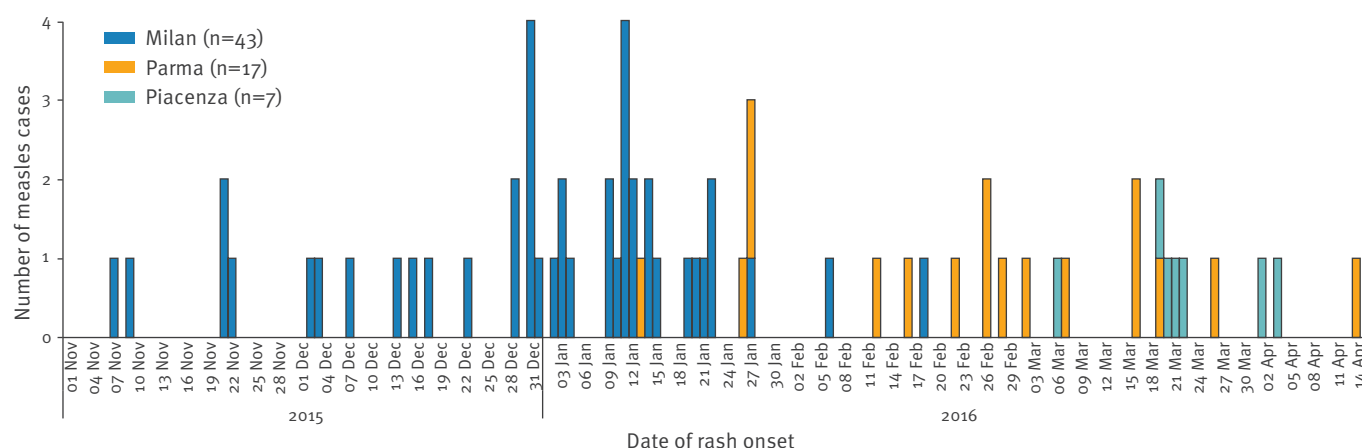
Staff of the local health authorities in Milan visited the three settlements on several occasions, together with cultural mediators, to identify contacts and search for additional cases. All persons 18 years or younger were invited to the vaccination centre for post-exposure prophylaxis. At the time of the visits, 54, 165 and 27 persons, respectively, were present in the three camps, of whom 52 (38 aged ≤18 years) received vaccination.

In Emilia Romagna, contacts were invited to be vaccinated. Overall 17 contacts were vaccinated (15 were older than 18 years).

In both regions, local health authorities informed local hospitals, emergency departments, family physicians/paediatricians and the local media of the outbreaks, and urged physicians to investigate all suspected measles cases, to isolate them if infectious and to notify

FIGURE 2

Number of reported measles cases by date of symptom onset, outbreak involving the Roma/Sinti population in Milan and spreading to Parma and Piacenza, Italy, November 2015–April 2016 (n = 67)



cases immediately. In Emilia Romagna, occupational physicians were reminded to implement the regional recommendation to verify measles immunity status of all unvaccinated hospital staff and staff of community healthcare services, and to offer vaccination to all those found to be susceptible. Results on uptake are pending at the time of publication.

Discussion

This outbreak highlights the immunity gaps existing in Roma/Sinti population groups and HCW in Italy. Both are considered to be hard-to-reach populations and outbreaks have also been reported in Europe and other industrialised countries [7–9].

The Roma people are a heterogeneous nomadic ethnic group who live in many countries worldwide but primarily in Europe. An estimated 140,000 Roma live in Italy (ca 3,400 in Milan). It is difficult to monitor uptake of measles-mumps-rubella vaccine among the Roma, but it is known to be low [9]. In this outbreak, a high level of susceptibility was found among children (median age of cases: 4 years), confirming a low vaccination uptake. Barriers to vaccination among the Roma have been previously described [9].

In Milan, the outbreak in the Roma settlement did not spread extensively in the community and no nosocomial cases were reported, despite the high number of cases that sought medical treatment. On the other hand, in Emilia Romagna, transmission occurred mainly in the nosocomial setting, suggesting that vaccination coverage is low among HCW in this region. In both regions, measles vaccination uptake in 2015 was above the national average but below the target of 95% for both doses (first-dose coverage in two-year old children 89.5% and 88.3%, respectively, in Lombardy and Emilia Romagna; second-dose coverage in six year-old children 91% in both regions) [10].

Despite a thorough investigation, no source of exposure was found for some cases in Parma and Piacenza and phylogenetic analysis was essential to confirm connections among cases. It is likely that not all cases were detected by the surveillance system, the sensitivity of which should be strengthened by raising awareness of measles among physicians and increasing the rate of suspected cases being tested. However, it is known that many measles cases do not seek health care and this may also have affected sensitivity. Some cases were initially misdiagnosed, probably because many clinicians are no longer familiar with the clinical presentation of measles. They need to be reminded to consider measles in the differential diagnosis of any febrile rash illness, especially in unvaccinated persons, and to immediately report suspected case to public health authorities so that control measures can be implemented rapidly.

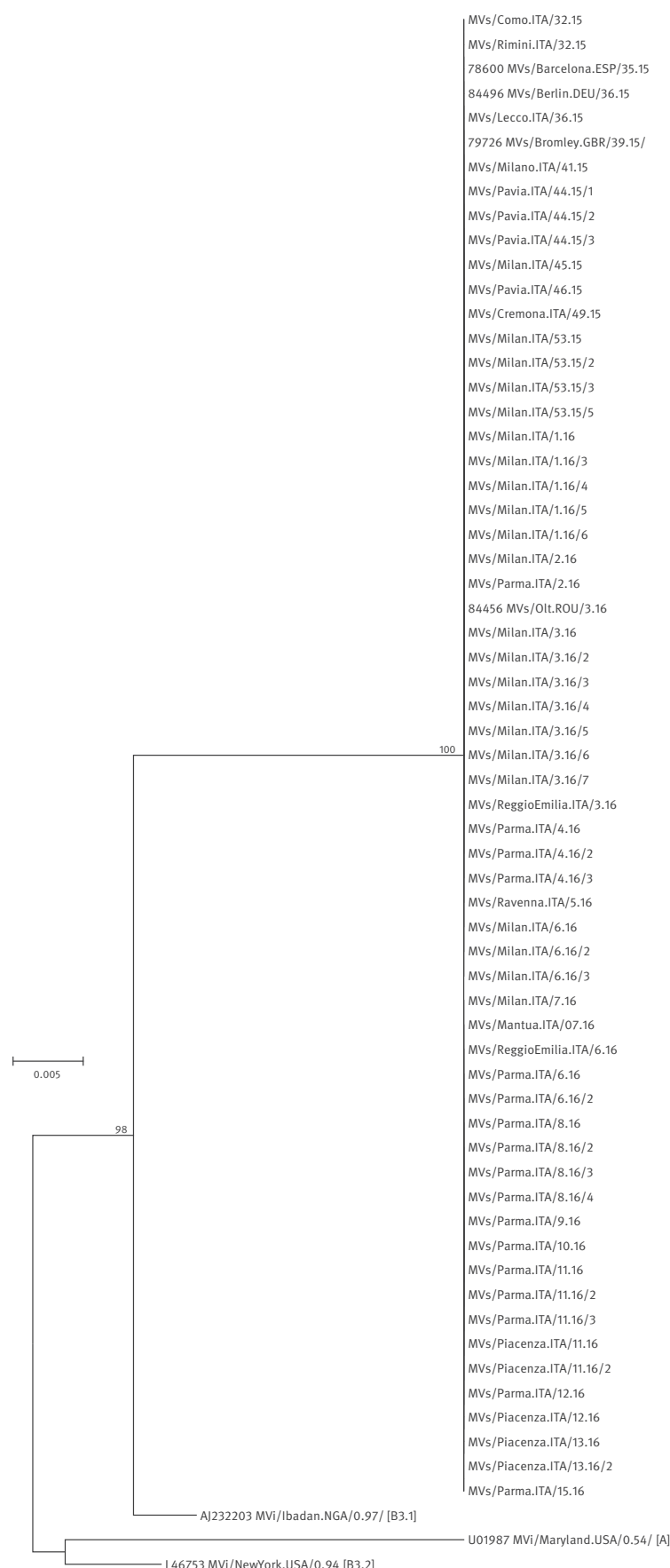
Three cases were detected among migrants living in one of the Roma settlements in Milan. It is possible that other undetected measles cases may have occurred among migrants living temporarily in the settlement. However, this is unlikely, as local health authorities, together with cultural mediators, visited the camp repeatedly during the outbreak and did not detect other cases. At the time of the outbreak, only a very small minority of persons living in one of the camps were migrants. These were persons of southern Asian and northern African origin who have access to medical care and immunisations in Italy.

MeaNS data from the last 12 months show that measles virus genotype B3 was endemic in several countries worldwide [6]. The appearance of a new B3 variant in Italy is probably due to importation, however, the route of introduction remains unknown.

To achieve measles elimination, besides strengthening surveillance and improving vaccination coverage in the general population, immunisation resources and

FIGURE 3

Neighbour-joining tree for nucleotide sequences of a new measles virus B3.1 variant causing an outbreak involving the Roma/Sinti population and the nosocomial setting, Italy, November 2015–April 2016 (n = 36)



The selected strains were aligned using BioEdit. Bayesian information criterion was used to determine the model of nucleotide substitution that best fit the data using the selection tool available in MEGA6. The model that best fit the data was the Kimura 2-parameter model.

tailored strategies should be directed at Roma communities and HCW. It has been suggested that greater vaccination uptake may be achieved among Roma children by inviting complete households for vaccination and by involving cultural mediators [11]. Also, control measures must be strengthened, including rapid case identification with implementation of airborne precautions in healthcare facilities to avoid nosocomial transmission [12].

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Conflict of interest

None declared.

Authors' contributions

A Filia coordinated surveillance activities and the epidemiological investigation and wrote the manuscript. A Amendola, S Bianchi, and E Tanzi performed genotyping and phylogenetic analysis of measles virus sequences isolated from cases in the Lombardy region and interpreted results. M Faccini, S Senatore, coordinated outbreak investigation and control activities in Milan (Lombardy). M Del Manso analysed data from the national measles surveillance system. A Ciampelli, MT Filippini carried out outbreak investigation activities in the nomadic camps. BM Borrini, MG Pascucci coordinated the epidemiological investigation in the Emilia Romagna region. T Lazzarotto, G Piccirilli performed genotyping and phylogenetic analysis of measles virus sequences isolated from cases in the Emilia Romagna region and interpreted the results. M Baggieri, F Magurano analysed measles virus sequences from the Lombardy and Emilia Romagna regions and performed phylogenetic analysis. F Magurano coordinated the virological investigation of the outbreak and supervised phylogenetic analyses. All authors reviewed and approved the final manuscript.

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